

# SEQUENCE LISTING

## (1) GENERAL INFORMATION:

- (i) APPLICANT: Lin, Lih-Ling  
Graham, James
- (ii) TITLE OF INVENTION: NOVEL INTERLEUKIN-1 RECEPTOR  
INTRACELLULAR LIGAND PROTEINS AND INHIBITORS OF LIGAND  
BINDING
- (iii) NUMBER OF SEQUENCES: 7
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: LEGAL AFFAIRS, GENETICS INSTITUTE, INC.
  - (B) STREET: 87 CambridgePark Drive
  - (C) CITY: Cambridge
  - (D) STATE: MA
  - (E) COUNTRY: USA
  - (F) ZIP: 02140
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Floppy disk
  - (B) COMPUTER: IBM PC compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER:
  - (B) FILING DATE:
  - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: Brown, Scott A.
  - (B) REGISTRATION NUMBER: 32,724
  - (C) REFERENCE/DOCKET NUMBER: GI5258
- (ix) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: (617) 498-8224
  - (B) TELEFAX: (617) 876-5851

## (2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1571 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 2..529

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

G ATC CCC AGG GTG GAC CTC CGG GTG TGG CAG GAC TGC TGT GAA GAC  
 Ile Pro Arg Val Asp Leu Arg Val Trp Gln Asp Cys Cys Glu Asp  
 1 5 10 15

46

TGT AGG ACC AGG GGG CAG TTC AAT GCC TTT TCC TAT CAT TTC CGA GGC Cys Arg Thr Arg Gly Gln Phe Asn Ala Phe Ser Tyr His Phe Arg Gly	20 25 30	94
AGA CGG TCT CTT GAG TTC AGC TAC CAG GAG GAC AAG CCG ACC AAG AAA Arg Arg Ser Leu Glu Phe Ser Tyr Gln Glu Asp Lys Pro Thr Lys Lys	35 40 45	142
ACA AGA CCA CGG AAA ATA CCC AGT GTT GGG AGA CAG GGG GAA CAT CTC Thr Arg Pro Arg Lys Ile Pro Ser Val Gly Arg Gln Gly Glu His Leu	50 55 60	190
AGC AAC AGC ACC TCA GCC TTC AGC ACA CGC TCA GAT GCA TCT GGG ACA Ser Asn Ser Thr Ser Ala Phe Ser Thr Arg Ser Asp Ala Ser Gly Thr	65 70 75	238
AAT GAC TTC AGA GAG TTT GTT CTG GAA ATG CAG AAG ACC ATC ACA GAC Asn Asp Phe Arg Glu Phe Val Leu Glu Met Gln Lys Thr Ile Thr Asp	80 85 90 95	286
CTC AGA ACA CAG ATA AAG AAA CTT GAA TCA CGG CTC AGT ACC ACA GAG Leu Arg Thr Gln Ile Lys Lys Leu Glu Ser Arg Leu Ser Thr Thr Glu	100 105 110	334
TGC GTG GAT GCC GGG GGC GAA TCT CAC GCC AAC AAC ACC AAG TGG AAA Cys Val Asp Ala Gly Gly Glu Ser His Ala Asn Asn Thr Lys Trp Lys	115 120 125	382
AAA GAT GCA TGC ACC ATT TGT GAA TGC AAA GAC GGG CAG GTC ACC TGC Lys Asp Ala Cys Thr Ile Cys Glu Cys Lys Asp Gly Gln Val Thr Cys	130 135 140	430
TTC GTG GAA GCT TGC CCC CCT GCC ACC TGT GCT GTC CCC GTG AAC ATC Phe Val Glu Ala Cys Pro Pro Ala Thr Cys Ala Val Pro Val Asn Ile	145 150 155	478
CCA GGG GCC TGC TGT CCA GTC TGC TTA CAG AAG AGG GCG GAG GAA AAG Pro Gly Ala Cys Cys Pro Val Cys Leu Gln Lys Arg Ala Glu Glu Lys	160 165 170 175	526
CCC TAGGCTCCTG GGAGGCTCCT CAGAGTTTGT CTGCTGTGCC ATCGTGAGAT Pro		579
CGGGTGGCCG ATGGCAGGGA GCTGCGGACT GCAGACCAGG AACACCCAG AACTCGTGAC		639
ATTTTCATGAC AACGTCACG TGGTGCTGTT ACAGAAGGCA GTGCAGGAGG CTTCCAACCA		699
GAGCATCTGC GGAGAAGGAG GCACAGCAGG TGCCCTGAAG GAAGCAGGCA GGAGTCCTAG		759
CTTCACGTTA GACTTCTCAG GTTTTTATT AATTCTTTTA AAATGAAAAA TTGCTGCTAC		819
TATTAATTG CACAGTTGAA TCATTTAGGC GCCTAAATTG ATTTTGCTCTC CCAACACCAT		879
TTCTTTTTAA ATAAAGCAGG ATACCTCTAT ATGTCAGCCT TGCCCTGTTC AGATGCCAGG		939
AGCCGGCAGA CCTGTCACCC GCAGGTGGGG TGAGTCTCGG AGCTGCCAGA GGGGCTCACC		999
GAAATCGGGG TTCCATCACA AGCTATGTTT AAAAAGAAAA TTGTGTGTTG CCAAACGGAA		1059
CAGAACCTTT GATGAGAGCG TTCACAGGGA CACTGTCTGG GGGTGCAGTG CAAGCCCCCG		1119
GCCTCTTCCC TGGGAACCTC TGAACCTCTC CTCTCTCTGG GCTCTCTGTA ACATTTCCAC		1179
ACACGTCAGC ATCTAATCCC AAGACAAACA TTCCCGCTGC TCGAAGCAGC TGTATAGCCT		1239
GTGACTCTCC GTGTGTCAGC TCCTTCCACA CCTGATTAG* ACATTCATAA GCCACATTTA		1299

GAAACAGGTT TGCTTTCAGC TGCTCACTGC ACACATACTG CCTAGTTGTG AACCAATGT 1359  
 GAAAAAACCT CCTTCATCCC ATTGTGTATC TGATACCTGC CGAGGGCCAA GGGTGTGTGT 1419  
 TGACAACGCC GCTCCCAGCC GGCCCTGGTT GCGTCCACGT CCTGAACAAG AGCCGCTTCC 1479  
 GGATGGCTCT TCCCAAGGGA GGAGGAGCTC AAGTGTGGG AACTGTCTAA CTTCAGGTTG 1539  
 TGTGAGTGGG TTAATAAAAA AAAAAAAA AA 1571

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 176 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Ile Pro Arg Val Asp Leu Arg Val Trp Gln Asp Cys Cys Glu Asp Cys  
 1 5 10 15  
 Arg Thr Arg Gly Gln Phe Asn Ala Phe Ser Tyr His Phe Arg Gly Arg  
 20 25 30  
 Arg Ser Leu Glu Phe Ser Tyr Gln Glu Asp Lys Pro Thr Lys Lys Thr  
 35 40 45  
 Arg Pro Arg Lys Ile Pro Ser Val Gly Arg Gln Gly Glu His Leu Ser  
 50 55 60  
 Asn Ser Thr Ser Ala Phe Ser Thr Arg Ser Asp Ala Ser Gly Thr Asn  
 65 70 75 80  
 Asp Phe Arg Glu Phe Val Leu Glu Met Gln Lys Thr Ile Thr Asp Leu  
 85 90 95  
 Arg Thr Gln Ile Lys Lys Leu Glu Ser Arg Leu Ser Thr Thr Glu Cys  
 100 105 110  
 Val Asp Ala Gly Gly Glu Ser His Ala Asn Thr Lys Trp Lys Lys  
 115 120 125  
 Asp Ala Cys Thr Ile Cys Glu Cys Lys Asp Gly Gln Val Thr Cys Phe  
 130 135 140  
 Val Glu Ala Cys Pro Pro Ala Thr Cys Ala Val Pro Val Asn Ile Pro  
 145 150 155 160  
 Gly Ala Cys Cys Pro Val Cys Leu Gln Lys Arg Ala Glu Glu Lys Pro  
 165 170 175

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1088 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

## (ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 2..961

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

G AAA AAA GGA GGT AAA ACA GAA CAG GAT GGC TAT CAG AAA CCC ACC Lys Lys Gly Gly Lys Thr Glu Gln Asp Gly Tyr Gln Lys Pro Thr 1 5 10 15	46
AAC AAA CAC TTC ACG CAG AGT CCC AAG AAG TCA GTG GCC GAC CTG CTG Asn Lys His Phe Thr Gln Ser Pro Lys Lys Ser Val Ala Asp Leu Leu 20 25 30	94
GGG TCC TTT GAA GGC AAA CGA AGA CTC CTT CTG ATC ACT GCT CCC AAG Gly Ser Phe Glu Gly Lys Arg Arg Leu Leu Ile Thr Ala Pro Lys 35 40 45	142
GCT GAG AAC AAT ATG TAT GTG CAA CAA CGT GAT GAA TAT CTG GAA AGT Ala Glu Asn Asn Met Tyr Val Gln Gln Arg Asp Glu Tyr Leu Glu Ser 50 55 60	190
TTC TGC AAG ATG GCT ACC AGG AAA ATC TCT GTG ATC ACC ATC TTC GGC Phe Cys Lys Met Ala Thr Arg Lys Ile Ser Val Ile Thr Ile Phe Gly 65 70 75	238
CCT GTC AAC AAC AGC ACC ATG AAA ATC GAC CAC TTT CAG CTA GAT AAT Pro Val Asn Asn Ser Thr Met Lys Ile Asp His Phe Gln Leu Asp Asn 80 85 90 95	286
GAG AAG CCC ATG CGA GTG GTG GAT GAT GAA GAC TTG GTA GAC CAG CGT Glu Lys Pro Met Arg Val Val Asp Asp Glu Asp Leu Val Asp Gln Arg 100 105 110	334
CTC ATC AGC GAG CTG AGG AAA GAG TAC GGA ATG ACC TAC AAT GAC TTC Leu Ile Ser Glu Leu Arg Lys Glu Tyr Gly Met Thr Tyr Asn Asp Phe 115 120 125	382
TTC ATG GTG CTA ACA GAT GTG GAT CTG AGA GTC AAG CAA TAC TAT GAG Phe Met Val Leu Thr Asp Val Asp Leu Arg Val Lys Gln Tyr Tyr Glu 130 135 140	430
GTA CCA ATA ACA ATG AAG TCT GTG TTT GAT CTG ATC GAT ACT TTC CAG Val Pro Ile Thr Met Lys Ser Val Phe Asp Leu Ile Asp Thr Phe Gln 145 150 155	478
TCC CGA ATC AAA GAT ATG GAG AAG CAG AAG AAG GAG GGC ATT GTT TGC Ser Arg Ile Lys Asp Met Glu Lys Gln Lys Lys Glu Gly Ile Val Cys 160 165 170 175	526
AAA GAG GAA GTT GGG GGA GTG TTA GAA CTG TTC CCA ATT AAT GGG AGC Lys Glu Glu Val Gly Gly Val Leu Glu Leu Phe Pro Ile Asn Gly Ser 180 185 190	574
TCT GTT GTT GAG CGA GAA GAC GTA CCA GCC CAT TTG GTG AAA GAC ATT Ser Val Val Glu Arg Glu Asp Val Pro Ala His Leu Val Lys Asp Ile 195 200 205	622
CGT AAC TAT TTT CAA GTG AGC CCG GAG TAC TTC TCC ATG CTT CTA GTC Arg Asn Tyr Phe Gln Val Ser Pro Glu Tyr Phe Ser Met Leu Leu Val 210 215 220	670
GGA AAA GAC GGA AAT GTC AAA TCC TGG TAT CCT TCC CCA ATG TGG TCC Gly Lys Asp Gly Asn Val Lys Ser Trp Tyr Pro Ser Pro Met Trp Ser 225 230 235	718

ATG GTG ATT GTG TAC GAT TTA ATT GAT TCG ATG CAA CTT CGG AGA CAG	766
Met Val Ile Val Tyr Asp Leu Ile Asp Ser Met Gln Leu Arg Arg Gln	
240 245 250 255	
GAA ATG GCG ATT CAG CAG TCA CTG GGG ATG CGC TGC CAG AAG ATG AGT	814
Glu Met Ala Ile Gln Gln Ser Leu Gly Met Arg Cys Gln Lys Met Ser	
260 265 270	
ATG CAG GCT ATG GTT ACC ATA GTT ACC ACC AAG GAT ACC AGG ATG GTT	862
Met Gln Ala Met Val Thr Ile Val Thr Thr Lys Asp Thr Arg Met Val	
275 280 285	
ACC AGG ATG ACT ACC GTC ATC ATG AGA GTT ATC ACC ATG GAT ACC CTT	910
Thr Arg Met Thr Thr Val Ile Met Arg Val Ile Thr Met Asp Thr Leu	
290 295 300	
ACT GAG CAG AAA TAT GTA ACC TTA GAC TCA GCC AGT TTC CTC TGC AGC	958
Thr Glu Gln Lys Tyr Val Thr Leu Asp Ser Ala Ser Phe Leu Cys Ser	
305 310 315	
TGC TAAACTACA TGTGGCCAGC TCCATTCTTC CACACTGCGT ACTACATTTT	1011
Cys	
320	
CTGCCTTTT CTTTCAGTGT TTTTCTAAGA CTAAATAAAT AGCAAACCTT CACCTAAAAA	1071
AAAAAAAAA AAAAAA	1088

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 320 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Lys	Lys	Gly	Gly	Lys	Thr	Glu	Gln	Asp	Gly	Tyr	Gln	Lys	Pro	Thr	Asn
1				5					10					15	
Lys	His	Phe	Thr	Gln	Ser	Pro	Lys	Lys	Ser	Val	Ala	Asp	Leu	Leu	Gly
	20						25						30		
Ser	Phe	Glu	Gly	Lys	Arg	Arg	Leu	Leu	Leu	Ile	Thr	Ala	Pro	Lys	Ala
	35					40					45				
Glu	Asn	Asn	Met	Tyr	Val	Gln	Gln	Arg	Asp	Glu	Tyr	Leu	Glu	Ser	Phe
	50				55				60						
Cys	Lys	Met	Ala	Thr	Arg	Lys	Ile	Ser	Val	Ile	Thr	Ile	Phe	Gly	Pro
	65				70				75					80	
Val	Asn	Asn	Ser	Thr	Met	Lys	Ile	Asp	His	Phe	Gln	Leu	Asp	Asn	Glu
			85					90					95		
Lys	Pro	Met	Arg	Val	Val	Asp	Asp	Glu	Asp	Leu	Val	Asp	Gln	Arg	Leu
		100					105					110			
Ile	Ser	Glu	Leu	Arg	Lys	Glu	Tyr	Gly	Met	Thr	Tyr	Asn	Asp	Phe	Phe
	115					120						125			
Met	Val	Leu	Thr	Asp	Val	Asp	Leu	Arg	Val	Lys	Gln	Tyr	Thr	Glu	Val
	130					135						140			

Pro Ile Thr Met Lys Ser Val Phe Asp Leu Ile Asp Thr Phe Gln Ser  
 145 150 155 160  
 Arg Ile Lys Asp Met Glu Lys Gln Lys Lys Glu Gly Ile Val Cys Lys  
 165 170 175  
 Glu Glu Val Gly Gly Val Leu Glu Leu Phe Pro Ile Asn Gly Ser Ser  
 180 185 190  
 Val Val Glu Arg Glu Asp Val Pro Ala His Leu Val Lys Asp Ile Arg  
 195 200 205  
 Asn Tyr Phe Gln Val Ser Pro Glu Tyr Phe Ser Met Leu Leu Val Gly  
 210 215 220  
 Lys Asp Gly Asn Val Lys Ser Trp Tyr Pro Ser Pro Met Trp Ser Met  
 225 230 235 240  
 Val Ile Val Tyr Asp Leu Ile Asp Ser Met Gln Leu Arg Arg Gln Glu  
 245 250 255  
 Met Ala Ile Gln Gln Ser Leu Gly Met Arg Cys Gln Lys Met Ser Met  
 260 265 270  
 Gln Ala Met Val Thr Ile Val Thr Thr Lys Asp Thr Arg Met Val Thr  
 275 280 285  
 Arg Met Thr Thr Val Ile Met Arg Val Ile Thr Met Asp Thr Leu Thr  
 290 295 300  
 Glu Gln Lys Tyr Val Thr Leu Asp Ser Ala Ser Phe Leu Cys Ser Cys  
 305 310 315 320

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1759 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

- (ix) FEATURE:  
 (A) NAME/KEY: CDS  
 (B) LOCATION: 2..754

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

C AAA AAC TTC TTC CTG ACG AAT CGC GCC AGG GAG CGC TCA GAC ACC 46  
 Lys Asn Phe Phe Leu Thr Asn Arg Ala Arg Glu Arg Ser Asp Thr  
 1 5 10  
 TTC ATC AAC CTC CGG GAG GTG CTC AAC CGC TTC AAG CTG CCG CCA GGA 94  
 Phe Ile Asn Leu Arg Glu Val Leu Asn Arg Phe Lys Leu Pro Pro Gly  
 20 25 30  
 GAG TAC ATT CTC GTG CCT TCC ACC TTC GAA CCC AAC AAG GAT GGG GAT 142  
 Glu Tyr Ile Leu Val Pro Ser Thr Phe Glu Pro Asn Lys Asp Gly Asp  
 35 40 45

TTC TGC ATC CGG GTC TTT TCT GAA AAG AAA GCT GAC TAC CAA GCT GTC Phe Cys Ile Arg Val Phe Ser Glu Lys Lys Ala Asp Tyr Gln Ala Val 50 55 60	190
GAT GAT GAA ATC GAG GCC AAT CTT GAA GAG TTC GAC ATC AGC GAG GAT Asp Asp Glu Ile Glu Ala Asn Leu Glu Glu Phe Asp Ile Ser Glu Asp 65 70 75	238
GAC ATT GAT GAT GGA TTC AGG AGA CTG TTT GCC CAG TTG GCA GGA GAG Asp Ile Asp Asp Gly Phe Arg Arg Leu Phe Ala Gln Leu Ala Gly Glu 80 85 90 95	286
GAT GCG GAG ATC TCT GCC TTT GAG CTG CAG ACC ATC CTG AGA AGG GTT Asp Ala Glu Ile Ser Ala Phe Glu Leu Gln Thr Ile Leu Arg Arg Val 100 105 110	334
CTA GCA AAG CGC CAA GAT ATC AAG TCA GAT GGC TTC AGC ATC GAG ACA Leu Ala Lys Arg Gln Asp Ile Lys Ser Asp Gly Phe Ser Ile Glu Thr 115 120 125	382
TGC AAA ATT ATG GTT GAC ATG CTA GAT TCG GAC GGG AGT GGC AAG CTG Cys Lys Ile Met Val Asp Met Leu Asp Ser Asp Gly Ser Gly Lys Leu 130 135 140	430
GGG CTG AAG GAG TTC TAC ATT CTC TGG ACG AAG ATT CAA AAA TAC CAA Gly Leu Lys Glu Phe Tyr Ile Leu Trp Thr Lys Ile Gln Lys Tyr Gln 145 150 155	478
AAA ATT TAC CGA GAA ATC GAC GTT GAC AGG TCT GGT ACC ATG AAT TCC Lys Ile Tyr Arg Glu Ile Asp Val Asp Arg Ser Gly Thr Met Asn Ser 160 165 170 175	526
TAT GAA ATG CGG AAG GCA TTA GAA GAA GCA GGT TTC AAG ATG CCC TGT Tyr Glu Met Arg Lys Ala Leu Glu Glu Ala Gly Phe Lys Met Pro Cys 180 185 190	574
CAA CTC CAC CAA GTC ATC GTT GCT CGG TTT GCA GAT GAC CAG CTC ATC Gln Leu His Gln Val Ile Val Ala Arg Phe Ala Asp Asp Gln Leu Ile 195 200 205	622
ATC GAT TTT GAT AAT TTT GTT CGG TGT TTG GTT CGG CTG GAA ACG CTA Ile Asp Phe Asp Asn Phe Val Arg Cys Leu Val Arg Leu Glu Thr Leu 210 215 220	670
TTC AAG ATA TTT AAG CAG CTG GAT CCC GAG AAT ACT GGA ACA ATA GAG Phe Lys Ile Phe Lys Gln Leu Asp Pro Glu Asn Thr Gly Thr Ile Glu 225 230 235	718
CTC GAC CTT ATC TCT TGG CTC TGT TTC TCA GTA CTT TGAAGTTATA Leu Asp Leu Ile Ser Trp Leu Cys Phe Ser Val Leu 240 245 250	764
ACTAATCTGC CTGAAGACTT CTCATGATGG AAAATCAGCC AAGGACTAAG CTTCATAGA	824
AATACACTTT GTATCTGGAC CTCAAAATTA TGGGAACATT TACTTAAACG GATGATCATA	884
GCTGAAAATA ATGATACTGT CAATTTGAGA TAGCAGAAGT TTCACACATC AAAGTAAAG	944
ATTGTCATAT CATTATACTA AATGCAATG AGTCGCTTAA CCCTTGACAA GGTCAAAGAA	1004
AGCTTTAAAT CTGTAATAG TATACACTTT TTACTTTTAC ACACCTTTCCT GTTCATAGCA	1064
ATATTAAATC AGGAAAAAAA AATGCAGGGA GGTATTTAAC AGCTGAGCAA AAACATTGAG	1124
TCGCTCTCAA AGGACACGAG GCCCTTGSCA GGGAAATATT AAGCAACTT CAAGTTTAAA	1184
ATGCAGCTGT TGATTCTACC AAACAACAGT CCAAGATTAC CATTTCCTAT GA3CCAAGCTG	1244

GGAAACATCG TATATCATGA AGTAATCTTG TCAAGGCATC TGGAGAGTCC AGGAGAGAAG	1304
ACTCACTCTC GTCGCTTGGG TTAACAAGA GACAGGTTTT GTAGAATATT GATTGGTAAT	1364
AGTAAATCGT TCTCCTTACA ATCAAGTTCT TGACCTATT CGGCCTTATA CATCTGGTCT	1424
TACAAAGACC AAAGGGATCC TCGCTTGAT CAACTGAACC AGTATGCCAA AACCAGGCAT	1484
CCAAATTGTA AACCAATTAT GATAAAGGAC AAAATAAGCT GTTTGCCACC TCAAACTTT	1544
ATGAACCTCA CCACCAC TAGTGTCTGTCCA TGGAGTTAGA GGGGACATCA CTTAGAAGTT	1604
CTTAGAGAAA GGACACAAGT TTGTTTCCTG GCTTTACCTT GGGAAAATGC TAGCAACATT	1664
ATAGAAATTT TGCCTTGTTG CCTTATCTTC TTCCAAATGT ACTGTTAAAT AAAAATAAAG	1724
GGTTACCCCA TGCAATCAAA AAAAAAAAAA AAAAA	1759

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 251 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Lys	Asn	Phe	Phe	Leu	Thr	Asn	Arg	Ala	Arg	Glu	Arg	Ser	Asp	Thr	Phe	
1					5				10					15		
Ile	Asn	Leu	Arg	Glu	Val	Leu	Asn	Arg	Phe	Lys	Leu	Pro	Pro	Gly	Glu	
		20						25					30			
Tyr	Ile	Leu	Val	Pro	Ser	Thr	Phe	Glu	Pro	Asn	Lys	Asp	Gly	Asp	Phe	
		35				40						45				
Cys	Ile	Arg	Val	Phe	Ser	Glu	Lys	Lys	Ala	Asp	Tyr	Gln	Ala	Val	Asp	
	50					55					60					
Asp	Glu	Ile	Glu	Ala	Asn	Leu	Glu	Glu	Phe	Asp	Ile	Ser	Glu	Asp	Asp	
	65				70				75					80		
Ile	Asp	Asp	Gly	Phe	Arg	Arg	Leu	Phe	Ala	Gln	Leu	Ala	Gly	Glu	Asp	
			85					90					95			
Ala	Glu	Ile	Ser	Ala	Phe	Glu	Leu	Gln	Thr	Ile	Leu	Arg	Arg	Val	Leu	
		100						105					110			
Ala	Lys	Arg	Gln	Asp	Ile	Lys	Ser	Asp	Gly	Phe	Ser	Ile	Glu	Thr	Cys	
		115				120					125					
Lys	Ile	Met	Val	Asp	Met	Leu	Asp	Ser	Asp	Gly	Ser	Gly	Lys	Leu	Gly	
	130					135					140					
Leu	Lys	Glu	Phe	Tyr	Ile	Leu	Trp	Thr	Lys	Ile	Gln	Lys	Tyr	Gln	Lys	
	145				150					155				160		
Ile	Tyr	Arg	Glu	Ile	Asp	Val	Asp	Arg	Ser	Gly	Thr	Met	Asn	Ser	Tyr	
		165						170					175			
Glu	Met	Arg	Lys	Ala	Leu	Glu	Glu	Ala	Gly	Phe	Lys	Met	Pro	Cys	Gln	
		180						185					190			



Leu His Gln Val Ile Val Ala Arg Phe Ala Asp Asp Gln Leu Ile Ile  
 195 200 205  
 Asp Phe Asp Asn Phe Val Arg Cys Leu Val Arg Leu Glu Thr Leu Phe  
 210 215 220  
 Lys Ile Phe Lys Gln Leu Asp Pro Glu Asn Thr Gly Thr Ile Glu Leu  
 225 230 235 240  
 Asp Leu Ile Ser Trp Leu Cys Phe Ser Val Leu  
 245 250

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 700 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met Ala Gly Ile Ala Ala Lys Leu Ala Lys Asp Arg Glu Ala Ala Glu  
 1 5 10 15  
 Gly Leu Gly Ser His Glu Arg Ala Ile Lys Tyr Leu Asn Gln Asp Tyr  
 20 25 30  
 Glu Ala Leu Arg Asn Glu Cys Leu Glu Ala Gly Thr Leu Phe Gln Asp  
 35 40 45  
 Pro Ser Phe Pro Ala Ile Pro Ser Ala Leu Gly Phe Lys Glu Leu Gly  
 50 55 60  
 Pro Tyr Ser Ser Lys Thr Arg Gly Met Arg Trp Lys Arg Pro Thr Glu  
 65 70 75 80  
 Ile Cys Ala Asp Pro Gln Phe Ile Ile Gly Gly Ala Thr Arg Thr Asp  
 85 90 95  
 Ile Cys Gln Gly Ala Leu Gly Asp Cys Trp Leu Leu Ala Ala Ile Ala  
 100 105 110  
 Ser Leu Thr Leu Asn Glu Glu Ile Leu Ala Arg Val Val Pro Leu Asn  
 115 120 125  
 Gln Ser Phe Gln Glu Asn Tyr Ala Gly Ile Phe His Phe Gln Phe Trp  
 130 135 140  
 Gln Tyr Gly Glu Trp Val Glu Val Val Val Asp Arg Leu Pro Thr  
 145 150 155 160  
 Lys Asp Gly Glu Leu Phe Val His Ser Ala Glu Gly Ser Glu Phe  
 165 170 175  
 Trp Ser Ala Leu Leu Glu Lys Ala Tyr Ala Lys Ile Asn Gly Cys Tyr  
 180 185 190  
 Glu Ala Leu Ser Gly Gly Ala Thr Thr Glu Gly Phe Glu Asp Phe Thr  
 195 200 205

Gly Gly Ile Ala Glu Trp Tyr Glu Leu Lys Lys Pro Pro Pro Asn Leu  
 210 215 220  
 Phe Lys Ile Ile Gln Lys Ala Leu Gln Lys Gly Ser Leu Leu Gly Cys  
 225 230 235 240  
 Ser Ile Asp Ile Thr Ser Ala Ala Asp Ser Glu Ala Ile Thr Phe Gln  
 245 250 255  
 Lys Leu Val Lys Gly His Ala Tyr Ser Val Thr Gly Ala Glu Glu Val  
 260 265 270  
 Glu Ser Asn Gly Ser Leu Gln Lys Leu Ile Arg Ile Arg Asn Pro Trp  
 275 280 285  
 Gly Glu Val Glu Trp Thr Gly Arg Trp Asn Asp Asn Cys Pro Ser Trp  
 290 295 300  
 Asn Thr Ile Asp Pro Glu Glu Arg Glu Arg Leu Thr Arg Arg His Glu  
 305 310 315 320  
 Asp Gly Glu Phe Trp Met Ser Phe Ser Asp Phe Leu Arg His Tyr Ser  
 325 330 335  
 Arg Leu Glu Ile Cys Asn Leu Thr Pro Asp Thr Leu Thr Ser Asp Thr  
 340 345 350  
 Tyr Lys Lys Trp Lys Leu Thr Lys Met Asp Gly Asn Trp Arg Arg Gly  
 355 360 365  
 Ser Thr Ala Gly Gly Cys Arg Asn Tyr Pro Asn Thr Phe Trp Met Asn  
 370 375 380  
 Pro Gln Tyr Leu Ile Lys Leu Glu Glu Glu Asp Glu Asp Glu Glu Asp  
 385 390 395 400  
 Gly Glu Ser Gly Cys Thr Phe Leu Val Gly Leu Ile Gln Lys His Arg  
 405 410 415  
 Arg Arg Gln Arg Lys Met Gly Glu Asp Met His Thr Ile Gly Phe Gly  
 420 425 430  
 Ile Tyr Glu Val Pro Glu Glu Leu Ser Gly Gln Thr Asn Ile His Leu  
 435 440 445  
 Ser Lys Asn Phe Phe Leu Thr Asn Arg Ala Arg Glu Arg Ser Asp Thr  
 450 455 460  
 Phe Ile Asn Leu Arg Glu Val Leu Asn Arg Phe Lys Leu Pro Pro Gly  
 465 470 475 480  
 Glu Tyr Ile Leu Val Pro Ser Thr Phe Glu Pro Asn Lys Asp Gly Asp  
 485 490 495  
 Phe Cys Ile Arg Val Phe Ser Glu Lys Lys Ala Asp Tyr Gln Ala Val  
 500 505 510  
 Asp Asp Glu Ile Glu Ala Asn Leu Glu Glu Phe Asp Ile Ser Glu Asp  
 515 520 525  
 Asp Ile Asp Asp Gly Val Arg Arg Leu Phe Ala Gln Leu Ala Gly Glu  
 530 535 540  
 Asp Ala Glu Ile Ser Ala Phe Glu Leu Gln Thr Ile Leu Arg Arg Val  
 545 550 555 560

Leu Ala Lys Arg Gln Asp Ile Lys Ser Asp Gly Phe Ser Ile Glu Thr  
 565 570 575  
 Cys Lys Ile Met Val Asp Met Leu Asp Ser Asp Gly Ser Gly Lys Leu  
 580 585 590  
 Gly Leu Lys Glu Phe Tyr Ile Leu Trp Thr Lys Ile Gln Lys Tyr Gln  
 595 600 605  
 Lys Ile Tyr Arg Glu Ile Asp Val Asp Arg Ser Gly Thr Met Asn Ser  
 610 615 620  
 Tyr Glu Met Arg Lys Ala Leu Glu Glu Ala Gly Phe Lys Met Pro Cys  
 625 630 635 640  
 Gln Leu His Gln Val Ile Val Ala Arg Phe Ala Asp Asp Gln Leu Ile  
 645 650 655  
 Ile Asp Phe Asp Asn Phe Val Arg Cys Leu Val Arg Leu Glu Thr Leu  
 660 665 670  
 Phe Lys Ile Phe Lys Gln Leu Asp Pro Glu Asn Thr Gly Thr Ile Glu  
 675 680 685  
 Leu Asp Leu Ile Ser Trp Leu Cys Phe Ser Val Leu  
 690 695 700